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<110> Weterings, Koen
Apuya, Nestor R.
Tatarinova, Tatiana
Goldberg, Robert B.
The Regents of the University of California

<120> Polynucleotides Useful for Modulating Transcription

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1 5

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ttt gtg aat ctg agt gaa gga aga aca gga gga gtt gca gaa gaa tat      5668
Phe Val Asn Leu Ser Glu Gly Arg Thr Gly Gly Val Ala Glu Glu Tyr
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Trp Lys Lys Met Met Lys Asn Glu Pro Leu Pro Glu Pro Ile Lys Glu
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ctt ctc aac aat cct ttt agg acc gca caa gag aga ttc atc cag aat      5764
Leu Leu Asn Asn Pro Phe Arg Thr Ala Gln Glu Arg Phe Ile Gln Asn
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Glu Glu Tyr Trp Lys Lys Met Met Lys Asn Glu Pro Leu Pro Glu Pro
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Ile Lys Glu Leu Leu Asn Asn Pro Phe Arg Thr Ala Gln Glu Arg Phe
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Asn Glu
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Phe Ser Met Ala Trp Val Leu Met Ala Phe Val Leu Phe Ala Asn Ser
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gct atg ccc aca aat gga tcc act gtt ggg gta aaa aac atg ttg ggt   3270
Ala Met Pro Thr Asn Gly Ser Thr Val Gly Val Lys Asn Met Leu Gly
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ggt aaa ttg atg cta aac gtt tta tgt ccc cat att gat aag caa cac   3318
Gly Lys Leu Met Leu Asn Val Leu Cys Pro His Ile Asp Lys Gln His
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att atc ccg aat ggt ggt tca ttt gag tgg aag tac aat ggt ggt gct   3366
Ile Ile Pro Asn Gly Gly Ser Phe Glu Trp Lys Tyr Asn Gly Gly Ala
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cca cca ata gga caa tca cca ttc atg tgt ttc ttt cgg tgg aat aat   3414
Pro Pro Ile Gly Gln Ser Pro Phe Met Cys Phe Phe Arg Trp Asn Asn
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gtt cat cac tcc ctt gat ctg tgt tca cca agc aag tat act ggt tgt   3462
Val His His Ser Leu Asp Leu Cys Ser Pro Ser Lys Tyr Thr Gly Cys
         90                  95                  100

gaa aat gcc att tgg gaa atc aaa gaa aag caa ttt tgt agg tac aga   3510
Glu Asn Ala Ile Trp Glu Ile Lys Glu Lys Gln Phe Cys Arg Tyr Arg
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ggt gga cct att aat tat ttt tgc tat gac tgg gat gat tag           3552
Gly Gly Pro Ile Asn Tyr Phe Cys Tyr Asp Trp Asp Asp
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		35					40					45			
Pro	His	Ile	Asp	Lys	Gln	His	Ile	Ile	Pro	Asn	Gly	Gly	Ser	Phe	Glu
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Trp	Lys	Tyr	Asn	Gly	Gly	Ala	Pro	Pro	Ile	Gly	Gln	Ser	Pro	Phe	Met
65					70					75					80
Cys	Phe	Phe	Arg	Trp	Asn	Asn	Val	His	His	Ser	Leu	Asp	Leu	Cys	Ser
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Pro	Ser	Lys	Tyr	Thr	Gly	Cys	Glu	Asn	Ala	Ile	Trp	Glu	Ile	Lys	Glu
			100					105					110		
Lys	Gln	Phe	Cys	Arg	Tyr	Arg	Gly	Gly	Pro	Ile	Asn	Tyr	Phe	Cys	Tyr
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1 5 10

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 15                  20                  25

att cca gtt ccc aac gat cca tca tca aca aat tct gtg ttt cct acc   1827
Ile Pro Val Pro Asn Asp Pro Ser Ser Thr Asn Ser Val Phe Pro Thr
 30                  35                  40                  45

tcg aaa aga acc gtg gaa atc aat aat gat ctc ggt aat cag cta acg   1875
Ser Lys Arg Thr Val Glu Ile Asn Asn Asp Leu Gly Asn Gln Leu Thr
                 50                  55                  60

tta ctg tat cat tgt aaa tca aaa gac gat gat tta ggt aac cgg act   1923
Leu Leu Tyr His Cys Lys Ser Lys Asp Asp Asp Leu Gly Asn Arg Thr
             65                  70                  75

ctg caa cca ggt gag tcg tgg tct ttt agt ttc ggg cgt caa ttc ttt   1971
Leu Gln Pro Gly Glu Ser Trp Ser Phe Ser Phe Gly Arg Gln Phe Phe
         80                  85                  90

gga agg acg ttg tat ttt tgt agt ttt agt tgg cca aat gaa tcg cat   2019
Gly Arg Thr Leu Tyr Phe Cys Ser Phe Ser Trp Pro Asn Glu Ser His
 95                 100                 105

tcg ttc gat ata tat aaa gac cat cga gat agc ggc ggt gat aac aag   2067
Ser Phe Asp Ile Tyr Lys Asp His Arg Asp Ser Gly Gly Asp Asn Lys
110                 115                 120                 125

tgc gag agc gac agg tgt gtg tgg aag ata aga aga aac gga cct tgt   2115
Cys Glu Ser Asp Arg Cys Val Trp Lys Ile Arg Arg Asn Gly Pro Cys
                130                 135                 140

agg ttt aac gat gaa acg aag cag ttt gat ctt tgt tat cct tgg aat   2163
Arg Phe Asn Asp Glu Thr Lys Gln Phe Asp Leu Cys Tyr Pro Trp Asn
            145                 150                 155

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Lys Ser Leu Tyr
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Pro Asn Asp Pro Ser Ser Thr Asn Ser Val Phe Pro Thr Ser Lys Arg
35 40 45
Thr Val Glu Ile Asn Asn Asp Leu Gly Asn Gln Leu Thr Leu Leu Tyr
50 55 60
His Cys Lys Ser Lys Asp Asp Asp Leu Gly Asn Arg Thr Leu Gln Pro
65 70 75 80
Gly Glu Ser Trp Ser Phe Ser Phe Gly Arg Gln Phe Phe Gly Arg Thr
85 90 95
Leu Tyr Phe Cys Ser Phe Ser Trp Pro Asn Glu Ser His Ser Phe Asp
100 105 110
Ile Tyr Lys Asp His Arg Asp Ser Gly Gly Asp Asn Lys Cys Glu Ser
115 120 125
Asp Arg Cys Val Trp Lys Ile Arg Arg Asn Gly Pro Cys Arg Phe Asn
130 135 140
Asp Glu Thr Lys Gln Phe Asp Leu Cys Tyr Pro Trp Asn Lys Ser Leu
145 150 155 160
Tyr

<210> 10
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
control region homologous repeat of Scarlet
Runner Bean G564 and C541 promoter region

<400> 10
gaaaagcgaa 10

<210> 11
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
control element homologous repeat of Scarlet
Runner Bean G564 promoter region

<400> 11
gaaaagtgaa 10

<210> 12
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:promoter
control element of Arabidopsis G564 ortholog
promoter region

<400> 12
gaaaagccaa 10

<210> 13
<211> 450
<212> DNA
<213> Phaseolus coccineus

<220>
<223> Scarlet Runner Bean G564 promoter (-921 to -662)
PLACE database Signal Scan search sequence

<400> 13
tgaaaagtga agaaaaccat gtaatgaaaa caaaatggca cgacaatcaa aaaaagtttt 60
cacgcaaaat tttcttcaaa atttataaca ttttcatgtt gtgtttgttt caaagcctag 120
aaaaacgaag agttactatt ggtaatgaaa agcgaagaaa accacataat aaaaacaaaa 180
tggcacgaca atcaagaaaa agttttcaca caaaactttt ttcaaaattt actatgttta 240
tttcgaaatt tagaaaaacg aagagttatt attagtaatg aaaagcgaag aaaactacgt 300
aataaaaaac aaaatggcac gacaataaaa aaagttttca cgcaaaattt tcttggtgcg 360
cagaaagtta tatatattaa ttaattaatt ttcatttact tttttccctt tttattttaa 420
agttaaatta ttattatttt catttaaaat 450

<210> 14
<211> 448
<212> DNA
<213> Phaseolus coccineus

<220>
<223> Scarlet Runner Bean G564 promoter (-921 to -662)
PlantCARE database Signal Scan search sequence

<400> 14
gaaaagtgaa gaaaaccatg taatgaaaac aaaatggcac gacaatcaaa aaaagttttc 60
acgcaaaatt ttcttcaaaa tttataacat tttcatgttg tgtttgtttc aaagcctaga 120
aaaacgaaga gttactattg gtaatgaaaa gcgaagaaaa ccacataata aaaacaaaat 180
ggcacgacaa tcaagaaaaa gttttcacac aaaacttttt tcaaaattta ctatgtttat 240
ttcgaaattt agaaaaacga agagttatta ttagtaatga aaagcgaaga aaactacgta 300
ataaaaaaca aaatggcacg acaataaaaa aagttttcac gcaaaatttt cttggtgcgc 360
agaaagttat atatattaat taattaattt tcatttactt ttttcccttt ttattttaaa 420
gttaaattat tattattttc atttaaaa 448

<210> 15
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:site #S000067
MARTBOX signal sequence promoter control element

<400> 15
ttwtwttwtt 10

<210> 16
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3-AF1 binding site promoter control element

<400> 16
aagagttatt 10

<210> 17
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Hordeum vulgare ABRE and Petroselinum crispum ACE promoter control element

<400> 17
actacgtaat 10

<210> 18
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Solanum tuberosum AT1-motif promoter control element

<400> 18
ttttatttta aa 12

<210> 19
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat promoter control element

<400> 19
gttttcttca 10

<210> 20
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat promoter control element

<400> 20
attttcttca

10

<210> 21
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat promoter control element

<400> 21
gttttcttcg

10

<210> 22
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat promoter control element

<400> 22
ttttttcttga

10

<210> 23
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat promoter control element

<400> 23
ttttttctaaa

10

<210> 24
<211> 10
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:TC-rich repeat promoter control element

<400> 24
attttcttgg

10

<210> 25
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide linker-primer

<400> 25
gagagagaga gagagagaga actagtctcg agttttttt ttttttttt 50

<210> 26
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anchor/reverse primer G primer

<400> 26
aagctttttt ttttg 16

<210> 27
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:anchor/reverse primer C primer

<400> 27
aagctttttt ttttc 16

<210> 28
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP49 forward primer

<400> 28
aagctttagt cca 13

<210> 29
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP50 forward primer

<400> 29
aagctttgag act 13

<210> 30
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP51 forward primer

<400> 30
aagcttcgaa atg

13

<210> 31
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP52 forward primer

<400> 31
aagcttgacc ttt

13

<210> 32
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP53 forward primer

<400> 32
aagcttcctc tat

13

<210> 33
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP54 forward primer

<400> 33
aagcttttga ggt

13

<210> 34
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP55 forward primer

<400> 34
aagcttacgt tag

13

<210> 35
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:H-AP56 forward primer

<400> 35
aagcttatga agg

13

<210> 36
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligo(dT-20) primer

<400> 36
tttttttttt tttttttttt

20

<210> 37
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:dT-20dN primer

<220>
<221> modified_base
<222> (21)
<223> n = g, c, a or t

<400> 37
tttttttttt tttttttttt n

21

<210> 38
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:mutagenic oligo

<400> 38
attggactgc atgcttacgc tagtctgtgc agag

34